

AKT3 Sequence Listings.ST25  
SEQUENCE LISTING

<110> Syrrx, Inc.  
 <120> CRYSTALLIZATION OF AKT3  
 <130> SYR-AKT3-5001-C1  
 <140> Not Yet Assigned  
 <141> 2003-06-20  
 <150> 60/400,207  
 <151> 2002-07-31  
 <160> 3  
 <170> PatentIn version 3.1  
 <210> 1  
 <211> 479  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> Amino acid sequence for full length human wild type AKT3  
 <222> (1)..(461)  
 <223>  
 <220>  
 <221> Amino acid sequence for full length human wild type AKT3  
 <222> (1)..(461)  
 <223> SEQ ID NO: 1 encodes for residues 136-461  
 <300>  
 <308> Genbank/NP\_005456  
 <309> 2002-04-04  
 <313> (1)..(461)  
 <400> 1  
 Met Ser Asp Val Thr Ile Val Lys Glu Gly Trp Val Gln Lys Arg Gly  
 1 5 10 15  
 Glu Tyr Ile Lys Asn Trp Arg Pro Arg Tyr Phe Leu Leu Lys Thr Asp  
 20 25 30  
 Gly Ser Phe Ile Gly Tyr Lys Glu Lys Pro Gln Asp Val Asp Leu Pro  
 35 40 45  
 Tyr Pro Leu Asn Asn Phe Ser Val Ala Lys Cys Gln Leu Met Lys Thr  
 50 55 60  
 Glu Arg Pro Lys Pro Asn Thr Phe Ile Ile Arg Cys Leu Gln Trp Thr  
 65 70 75 80  
 Thr Val Ile Glu Arg Thr Phe His Val Asp Thr Pro Glu Glu Arg Glu  
 85 90 95

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Glu Trp Thr Glu Ala Ile Gln Ala Val Ala Asp Arg Leu Gln Arg Gln  
100 105 110

Glu Glu Glu Arg Met Asn Cys Ser Pro Thr Ser Gln Ile Asp Asn Ile  
115 120 125

Gly Glu Glu Glu Met Asp Ala Ser Thr Thr His His Lys Arg Lys Thr  
130 135 140

Met Asn Asp Phe Asp Tyr Leu Lys Leu Leu Gly Lys Gly Thr Phe Gly  
145 150 155 160

Lys Val Ile Leu Val Arg Glu Lys Ala Ser Gly Lys Tyr Tyr Ala Met  
165 170 175

Lys Ile Leu Lys Lys Glu Val Ile Ile Ala Lys Asp Glu Val Ala His  
180 185 190

Thr Leu Thr Glu Ser Arg Val Leu Lys Asn Thr Arg His Pro Phe Leu  
195 200 205

Thr Ser Leu Lys Tyr Ser Phe Gln Thr Lys Asp Arg Leu Cys Phe Val  
210 215 220

Met Glu Tyr Val Asn Gly Gly Glu Leu Phe Phe His Leu Ser Arg Glu  
225 230 235 240

Arg Val Phe Ser Glu Asp Arg Thr Arg Phe Tyr Gly Ala Glu Ile Val  
245 250 255

Ser Ala Leu Asp Tyr Leu His Ser Gly Lys Ile Val Tyr Arg Asp Leu  
260 265 270

Lys Leu Glu Asn Leu Met Leu Asp Lys Asp Gly His Ile Lys Ile Thr  
275 280 285

Asp Phe Gly Leu Cys Lys Glu Gly Ile Thr Asp Ala Ala Thr Met Lys  
290 295 300

Thr Phe Cys Gly Thr Pro Glu Tyr Leu Ala Pro Glu Val Leu Glu Asp  
305 310 315 320

Asn Asp Tyr Gly Arg Ala Val Asp Trp Trp Gly Leu Gly Val Val Met  
325 330 335

Tyr Glu Met Met Cys Gly Arg Leu Pro Phe Tyr Asn Gln Asp His Glu  
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340

345

350

Lys Leu Phe Glu Leu Ile Leu Met Glu Asp Ile Lys Phe Pro Arg Thr  
355 360 365

Leu Ser Ser Asp Ala Lys Ser Leu Leu Ser Gly Leu Leu Ile Lys Asp  
370 375 380

Pro Asn Lys Arg Leu Gly Gly Gly Pro Asp Asp Ala Lys Glu Ile Met  
385 390 395 400

Arg His Ser Phe Phe Ser Gly Val Asn Trp Gln Asp Val Tyr Asp Lys  
405 410 415

Lys Leu Val Pro Pro Phe Lys Pro Gln Val Thr Ser Glu Thr Asp Thr  
420 425 430

Arg Tyr Phe Asp Glu Glu Phe Thr Ala Gln Thr Ile Thr Ile Thr Pro  
435 440 445

Pro Glu Lys Tyr Asp Glu Asp Gly Met Asp Cys Met Asp Asn Glu Arg  
450 455 460

Arg Pro His Phe Pro Gln Phe Ser Tyr Ser Ala Ser Gly Arg Glu  
465 470 475

<210> 2  
<211> 978  
<212> DNA  
<213> Homo sapiens

<220>  
<221> Human cDNA sequence encoding residues 136-461 of AKT3  
<222> (1)..(978)  
<223>

<400> 2  
tctacaaccc atcataaaag aaagacaatg aatgattttg actatttgaa actactaggt 60  
aaaggcactt ttgggaaagt tattttggtt cgagagaagg caagtggaaa atactatgct 120  
atgaagattc tgaagaaaga agtcattatt gcaaaggatg aagtggcaca cactctaact 180  
gaaagcagag tattaagaa cactagacat ccctttttaa catccttgaa atattccttc 240  
cagacaaaag accgtttgtg ttttgtgatg gaatatgtta atgggggcca gctgtttttc 300  
catttgtcga gagagcgggt gttctctgag gaccgcacac gtttctatgg tgcagaaatt 360  
gtctctgcct tggactatct acattccgga aagattgtgt accgtgatct caagttggag 420  
aatctaattg tggacaaaga tggccacata aaaattacag attttggact ttgcaaagaa 480  
gggatcacag atgcagccac catgaagaca ttctgtggca ctccagaata tctggcacca 540

# AKT3 Sequence Listings.ST25

```

gaggtgtag aagataatga ctatggccga gcagtagact ggtggggcct aggggttgtc 600
atgtatgaaa tgatgtgtgg gaggttacct ttctacaacc aggaccatga gaaacttttt 660
gaattaatat taatggaaga cattaatttt cctcgaacac tctcttcaga tgcaaaatca 720
ttgctttcag ggctcttgat aaaggatcca aataaacgcc ttggtggagg accagatgat 780
gcaaaagaaa ttatgagaca cagtttcttc tctggagtaa actggcaaga tgtatatgat 840
aaaaagcttg tacctccttt taaacctcaa gtaacatctg agacagatac tagatatttt 900
gatgaagaat ttacagctca gactattaca ataaccaccac ctgaaaaata tgatgaggat 960
ggtatggact gcatggac 978

```

```

<210> 3
<211> 556
<212> PRT
<213> Homo sapiens

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<220>
<221> Amino Acid Sequence for residues 136-461
<222> (1)..(556)
<223>

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<220>
<221> Amino Acid Sequence for residues 136-461
<222> (1)..(556)
<223> Cleavable intein tag and cleavage site (residues 1-226). Residues
227-230 (CRSL) is left on N-terminal post cleavage

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```

<400> 3

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Met Lys Ile Glu Glu Gly Lys Leu Thr Asn Pro Gly Val Ser Ala Trp
1 5 10 15

```

```

Gln Val Asn Thr Ala Tyr Thr Ala Gly Gln Leu Val Thr Tyr Asn Gly
20 25 30

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```

Lys Thr Tyr Lys Cys Leu Gln Pro His Thr Ser Leu Ala Gly Trp Glu
35 40 45

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```

Pro Ser Asn Val Pro Ala Leu Trp Gln Leu Gln Asn Asn Gly Asn Asn
50 55 60

```

```

Gly Leu Glu Leu Arg Glu Ser Gly Ala Ile Ser Gly Asp Ser Leu Ile
65 70 75 80

```

```

Ser Leu Ala Ser Thr Gly Lys Arg Val Ser Ile Lys Asp Leu Leu Asp
85 90 95

```

```

Glu Lys Asp Phe Glu Ile Trp Ala Ile Asn Glu Gln Thr Met Lys Leu
100 105 110

```

# AKT3 Sequence Listings.ST25

Glu Ser Ala Lys Val Ser Arg Val Phe Cys Thr Gly Lys Lys Leu Val  
115 120 125

Tyr Ile Leu Lys Thr Arg Leu Gly Arg Thr Ile Lys Ala Thr Ala Asn  
130 135 140

His Arg Phe Leu Thr Ile Asp Gly Trp Lys Arg Leu Asp Glu Leu Ser  
145 150 155 160

Leu Lys Glu His Ile Ala Leu Pro Arg Lys Leu Glu Ser Ser Ser Leu  
165 170 175

Gln Leu Ser Pro Glu Ile Glu Lys Leu Ser Gln Ser Asp Ile Tyr Trp  
180 185 190

Asp Ser Ile Val Ser Ile Thr Glu Thr Gly Val Glu Glu Val Phe Asp  
195 200 205

Leu Thr Val Pro Gly Pro His Asn Phe Val Ala Asn Asp Ile Ile Val  
210 215 220

His Asn Cys Arg Ser Leu Ser Thr Thr His His Lys Arg Lys Thr Met  
225 230 235 240

Asn Asp Phe Asp Tyr Leu Lys Leu Leu Gly Lys Gly Thr Phe Gly Lys  
245 250 255

Val Ile Leu Val Arg Glu Lys Ala Ser Gly Lys Tyr Tyr Ala Met Lys  
260 265 270

Ile Leu Lys Lys Glu Val Ile Ile Ala Lys Asp Glu Val Ala His Thr  
275 280 285

Leu Thr Glu Ser Arg Val Leu Lys Asn Thr Arg His Pro Phe Leu Thr  
290 295 300

Ser Leu Lys Tyr Ser Phe Gln Thr Lys Asp Arg Leu Cys Phe Val Met  
305 310 315 320

Glu Tyr Val Asn Gly Gly Glu Leu Phe Phe His Leu Ser Arg Glu Arg  
325 330 335

Val Phe Ser Glu Asp Arg Thr Arg Phe Tyr Gly Ala Glu Ile Val Ser  
340 345 350

Ala Leu Asp Tyr Leu His Ser Gly Lys Ile Val Tyr Arg Asp Leu Lys  
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355  
 360  
 365  
 Leu Glu Asn Leu Met Leu Asp Lys Asp Gly His Ile Lys Ile Thr Asp  
 370 375 380  
 Phe Gly Leu Cys Lys Glu Gly Ile Thr Asp Ala Ala Thr Met Lys Thr  
 385 390 395 400  
 Phe Cys Gly Thr Pro Glu Tyr Leu Ala Pro Glu Val Leu Glu Asp Asn  
 405 410 415  
 Asp Tyr Gly Arg Ala Val Asp Trp Trp Gly Leu Gly Val Val Met Tyr  
 420 425 430  
 Glu Met Met Cys Gly Arg Leu Pro Phe Tyr Asn Gln Asp His Glu Lys  
 435 440 445  
 Leu Phe Glu Leu Ile Leu Met Glu Asp Ile Lys Phe Pro Arg Thr Leu  
 450 455 460  
 Ser Ser Asp Ala Lys Ser Leu Leu Ser Gly Leu Leu Ile Lys Asp Pro  
 465 470 475 480  
 Asn Lys Arg Leu Gly Gly Gly Pro Asp Asp Ala Lys Glu Ile Met Arg  
 485 490 495  
 His Ser Phe Phe Ser Gly Val Asn Trp Gln Asp Val Tyr Asp Lys Lys  
 500 505 510  
 Leu Val Pro Pro Phe Lys Pro Gln Val Thr Ser Glu Thr Asp Thr Arg  
 515 520 525  
 Tyr Phe Asp Glu Glu Phe Thr Ala Gln Thr Ile Thr Ile Thr Pro Pro  
 530 535 540  
 Glu Lys Tyr Asp Glu Asp Gly Met Asp Cys Met Asp  
 545 550 555